

SEQUENCE LISTING

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 Immunex Corporation
 Cornell Research Foundation, Inc.

<120> Methods of Inhibiting Platelet Activation and
 Recruitment

<130> 23,495 USA

<140> US 09/807,660
 <141> 2001-09-06

<150> US 60/104,585
 <151> 1998-10-16

<150> US 60/107,466
 <151> 1998-11-06

<150> US 60/149,010
 <151> 1999-08-13

<160> 37

<170> PatentIn version 3.1

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 <222> (67)..(1596)

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 1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
 15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
 35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 50 55 60

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 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 80 85 90

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 95 100 105 110

aga Arg	gct Ala	agg Arg	gaa Glu	gtg Val 115	att Ile	cca Pro	agg Arg	tcc Ser	cag Gln 120	cac His	caa Gln	gag Glu	aca Thr	ccc Pro 125	gtt Val	444
tac Tyr	ctg Leu	gga Gly	gcc Ala 130	acg Thr	gca Ala	ggc Gly	atg Met	cgg Arg 135	ttg Leu	ctc Leu	agg Arg	atg Met	gaa Glu 140	agt Ser	gaa Glu	492
gag Glu	ttg Leu	gca Ala 145	gac Asp	agg Arg	gtt Val	ctg Leu	gat Asp 150	gtg Val	gtg Val	gag Glu	agg Arg	agc Ser 155	ctc Leu	agc Ser	aac Asn	540
tac Tyr	ccc Pro 160	ttt Phe	gac Asp	ttc Phe	cag Gln	ggc Gly 165	gcc Ala	agg Arg	atc Ile	att Ile	act Thr 170	ggc Gly	caa Gln	gag Glu	gaa Glu	588
ggt Gly 175	gcc Ala	tat Tyr	ggc Gly	tgg Trp	att Ile 180	act Thr	atc Ile	aac Asn	tat Tyr	ctg Leu 185	ctg Leu	ggc Gly	aaa Lys	ttc Phe	agt Ser 190	636
cag Gln	aaa Lys	aca Thr	agg Arg	tgg Trp 195	ttc Phe	agc Ser	ata Ile	gtc Val	cca Pro 200	tat Tyr	gaa Glu	acc Thr	aat Asn 205	aat Asn 205	cag Gln	684
gaa Glu	acc Thr	ttt Phe	gga Gly 210	gct Ala	ttg Leu	gac Asp	ctt Leu	ggg Gly 215	gga Gly	gcc Ala	tct Ser	aca Thr	caa Gln 220	gtc Val	act Thr	732
ttt Phe	gta Val	ccc Pro 225	caa Gln	aac Asn	cag Gln	act Thr	atc Ile 230	gag Glu	tcc Ser	cca Pro	gat Asp	aat Asn 235	gct Ala	ctg Leu	caa Gln	780
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tgc Cys 255	tat Tyr	ggg Gly	aag Lys	gat Asp	cag Gln 260	gca Ala	ctc Leu	tgg Trp	cag Gln	aaa Lys 265	ctg Leu	gcc Ala	aag Lys	gac Asp	att Ile 270	876
cag Gln	gtt Val	gca Ala	agt Ser	aat Asn 275	gaa Glu	att Ile	ctc Leu	agg Arg	gac Asp 280	cca Pro	tgc Cys	ttt Phe	cat His	cct Pro 285	gga Gly	924
tat Tyr	aag Lys	aag Lys	gta Val 290	gtg Val	aac Asn	gta Val	agt Ser	gac Asp 295	ctt Leu	tac Tyr	aag Lys	acc Thr	ccc Pro 300	tgc Cys	acc Thr	972
aag Lys	aga Arg	ttt Phe 305	gag Glu	atg Met	act Thr	ctt Leu	cca Pro 310	ttc Phe	cag Gln	cag Gln	ttt Phe	gaa Glu 315	atc Ile	cag Gln	ggc Gly	1020
att Ile	gga Gly 320	aac Asn	tat Tyr	caa Gln	caa Gln	tgc Cys 325	cat His	caa Gln	agc Ser	atc Ile	ctg Leu 330	gag Glu	ctc Leu	ttc Phe	aac Asn	1068
acc Thr 335	agt Ser	tac Tyr	tgc Cys	cct Pro	tac Tyr 340	tcc Ser	cag Gln	tgt Cys	gcc Ala	ttc Phe 345	aat Asn	ggg Gly	att Ile	ttc Phe	ttg Leu 350	1116
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atg Met	aag Lys	ttt Phe	tta Leu 370	aac Asn	ttg Leu	aca Thr	tca Ser	gag Glu 375	aaa Lys	gtc Val	tct Ser	cag Gln	gaa Glu 380	aag Lys	gtg Val	1212
act	gag	atg	atg	aaa	aag	ttc	tgt	gct	cag	cct 2	tgg	gag	gag	ata	aaa	1260

Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys		
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aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	1308	
Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe		
		400				405					410						
tct	ggt	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	1356	
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr		
					420					425					430		
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1404	
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser		
				435					440					445			
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1452	
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile		
			450					455					460				
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	tat	gtc	1500	
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val		
		465					470					475					
ttc	ctc	atg	ggt	cta	ttc	tcc	ctg	gtc	ctt	ttc	aca	gtg	gcc	atc	ata	1548	
Phe	Leu	Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile		
		480				485					490						
ggc	ttg	ctt	atc	ttt	cac	aag	cct	tca	tat	ttc	tgg	aaa	gat	atg	gta	1596	
Gly	Leu	Leu	Ile	Phe	His	Lys	Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val		
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tag																1599	

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 <213> Homo sapiens

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 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
 35 40 45
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
 100 105 110
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
 115 120 125
 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160
 3

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190
Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205
Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220
Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255
Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270
Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285
Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300
Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320
Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335
Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350
Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365
Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380
Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400
Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415
Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430
Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445
Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460
Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
465 470 475 480
Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
485 490 495
Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
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<211> 476
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

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 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
 35 40 45
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
 100 105 110
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
 115 120 125
 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
 165 170 175
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
 180 185 190
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
 195 200 205
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
 210 215 220
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
 225 230 235 240
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
 245 250 255
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
 260 265 270
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
 275 280 285
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
 290 295 300
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
 305 310 315 320

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
 165 170 175
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
 180 185 190
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
 195 200 205
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
 210 215 220
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
 225 230 235 240
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
 245 250 255
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
 260 265 270
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
 275 280 285
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
 290 295 300
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
 305 310 315 320
 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
 325 330 335
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
 340 345 350
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
 355 360 365
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
 370 375 380
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
 385 390 395 400
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
 405 410 415
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

8

aat Asn 225	gtc Val	tac Tyr	aca Thr	cat His	agc Ser 230	ttc Phe	ttg Leu	tgc Cys	tat Tyr	ggg Gly 235	aag Lys	gat Asp	cag Gln	gca Ala	ctc Leu 240	720
tg Trp	gag Gln	aaa Lys	ctg Leu	gcc Ala 245	aag Lys	gac Asp	att Ile	cag Gln	gtt Val 250	gca Ala	agt Ser	aat Asn	gaa Glu	att Ile 255	ctc Leu	768
agg Arg	gac Asp	cca Pro	tgc Cys 260	ttt Phe	cat His	cct Pro	gga Gly	tat Tyr 265	aag Lys	aag Lys	gta Val	gtg Val	aac Asn 270	gta Val	agt Ser	816
gac Asp	ctt Leu	tac Tyr 275	aag Lys	acc Thr	ccc Pro	tgc Cys	acc Thr 280	aag Lys	aga Arg	ttt Phe	gag Glu	atg Met 285	act Thr	ctt Leu	cca Pro	864
ttc Phe	cag Gln 290	cag Gln	ttt Phe	gaa Glu	atc Ile	cag Gln 295	ggt Gly	att Ile	gga Gly	aac Asn	tat Tyr 300	caa Gln	caa Gln	tgc Cys	cat His	912
caa Gln 305	agc Ser	atc Ile	ctg Leu	gag Glu	ctc Leu 310	ttc Phe	aac Asn	acc Thr	agt Ser	tac Tyr 315	tgc Cys	cct Pro	tac Tyr	tcc Ser	cag Gln 320	960
tgt Cys	gcc Ala	ttc Phe	aat Asn	ggg Gly 325	att Ile	ttc Phe	ttg Leu	cca Pro	cca Pro 330	ctc Leu	cag Gln	ggg Gly	gat Asp	ttt Phe 335	ggg Gly	1008
gca Ala	ttt Phe	tca Ser	gct Ala 340	ttt Phe	tac Tyr	ttt Phe	gtg Val	atg Met 345	aag Lys	ttt Phe	tta Leu	aac Asn	ttg Leu 350	aca Thr	tca Ser	1056
gag Glu	aaa Lys	gtc Val 355	tct Ser	cag Gln	gaa Glu	aag Lys	gtg Val 360	act Thr	gag Glu	atg Met	atg Met	aaa Lys 365	aag Lys	ttc Phe	tgt Cys	1104
gct Ala 370	cag Gln	cct Pro	tg Trp	gag Glu	gag Glu	ata Ile 375	aaa Lys	aca Thr	tct Ser	tac Tyr	gct Ala 380	gga Gly	gta Val	aag Lys	gag Glu	1152
aag Lys 385	tac Tyr	ctg Leu	agt Ser	gaa Glu	tac Tyr 390	tgc Cys	ttt Phe	tct Ser	ggt Gly	acc Thr 395	tac Tyr	att Ile	ctc Leu	tcc Ser	ctc Leu 400	1200
ctt Leu	ctg Leu	caa Gln	ggc Gly	tat Tyr 405	cat His	ttc Phe	aca Thr	gct Ala	gat Asp 410	tcc Ser	tg Trp	gag Glu	cac His	atc Ile 415	cat His	1248
ttc Phe	att Ile	ggc Gly	aag Lys 420	atc Ile	cag Gln	ggc Gly	agc Ser	gac Asp 425	gcc Ala	ggc Gly	tg Trp	act Thr	ttg Leu 430	ggc Gly	tac Tyr	1296
atg Met	ctg Leu	aac Asn 435	ctg Leu	acc Thr	aac Asn	atg Met	atc Ile 440	cca Pro	gct Ala	gag Glu	caa Gln	cca Pro 445	ttg Leu	tcc Ser	aca Thr	1344
cct Pro	ctc Leu	tcc Ser	cac His	tcc Ser	acc Thr	taa										1365

<210> 6

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion

construct of human CD39

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Gln Asn Lys Ala₂₀ Leu Pro Glu Asn Val₂₅ Lys Tyr Gly Ile Val₃₀ Leu Asp
Ala Gly Ser₃₅ Ser His Thr Ser Leu₄₀ Tyr Ile Tyr Lys Trp₄₅ Pro Ala Glu
Lys Glu₅₀ Asn Asp Thr Gly Val₅₅ Val His Gln Val Glu₆₀ Glu Cys Arg Val
Lys₆₅ Gly Pro Gly Ile Ser₇₀ Lys Phe Val Gln Lys₇₅ Val Asn Glu Ile Gly₈₀
Ile Tyr Leu Thr Asp₈₅ Cys Met Glu Arg Ala₉₀ Arg Glu Val Ile Pro₉₅ Arg
Ser Gln His Gln₁₀₀ Glu Thr Pro Val Tyr₁₀₅ Leu Gly Ala Thr Ala₁₁₀ Gly Met
Arg Leu Leu₁₁₅ Arg Met Glu Ser Glu₁₂₀ Glu Leu Ala Asp Arg₁₂₅ Val Leu Asp
Val Val₁₃₀ Glu Arg Ser Leu Ser₁₃₅ Asn Tyr Pro Phe Asp₁₄₀ Phe Gln Gly Ala
Arg₁₄₅ Ile Ile Thr Gly Gln₁₅₀ Glu Glu Gly Ala Tyr₁₅₅ Gly Trp Ile Thr Ile₁₆₀
Asn Tyr Leu Leu Gly₁₆₅ Lys Phe Ser Gln Lys₁₇₀ Thr Arg Trp Phe Ser₁₇₅ Ile
Val Pro Tyr Glu₁₈₀ Thr Asn Asn Gln Glu₁₈₅ Thr Phe Gly Ala Leu₁₉₀ Asp Leu
Gly Gly Ala₁₉₅ Ser Thr Gln Val Thr₂₀₀ Phe Val Pro Gln Asn₂₀₅ Gln Thr Ile
Glu Ser₂₁₀ Pro Asp Asn Ala Leu₂₁₅ Gln Phe Arg Leu Tyr₂₂₀ Gly Lys Asp Tyr
Asn Val₂₂₅ Tyr Thr His Ser₂₃₀ Phe Leu Cys Tyr Gly₂₃₅ Lys Asp Gln Ala Leu₂₄₀
Trp Gln Lys Leu Ala₂₄₅ Lys Asp Ile Gln Val₂₅₀ Ala Ser Asn Glu Ile₂₅₅ Leu
Arg Asp Pro Cys₂₆₀ Phe His Pro Gly Tyr₂₆₅ Lys Lys Val Val₂₇₀ Asn Val Ser
Asp Leu Tyr₂₇₅ Lys Thr Pro Cys Thr₂₈₀ Lys Arg Phe Glu Met₂₈₅ Thr Leu Pro
Phe Gln₂₉₀ Gln Phe Glu Ile Gln₂₉₅ Gly Ile Gly Asn Tyr₃₀₀ Gln Gln Cys His
Gln Ser₃₀₅ Ile Leu Glu Leu₃₁₀ Phe Asn Thr Ser Tyr₃₁₅ Cys Pro Tyr Ser Gln₃₂₀
Cys Ala Phe Asn Gly₃₂₅ Ile Phe Leu Pro Pro₃₃₀ Leu Gln Gly Asp Phe₃₃₅ Gly
Ala Phe Ser Ala₃₄₀ Phe Tyr Phe Val Met₃₄₅ Lys Phe Leu Asn Leu₃₅₀ Thr Ser

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
 355 360 365
 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
 370 375 380
 Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
 385 390 395 400

 Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
 405 410 415
 Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
 420 425 430
 Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
 435 440 445
 Pro Leu Ser His Ser Thr
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<220>
 <221> CDS
 <222> (1)..(1434)

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 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
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 agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

 aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac 144
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
 35 40 45

 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 192
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 50 55 60

 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 240
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75 80

 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 288
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 85 90 95

 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 336
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 100 105 110

 aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 384
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
 115 120 125

tac Tyr	ctg Leu 130	gga Gly	gcc Ala	acg Thr	gca Ala	ggc Gly 135	atg Met	cgg Arg	ttg Leu	ctc Leu	agg Arg 140	atg Met	gaa Glu	agt Ser	gaa Glu	432
gag Glu 145	ttg Leu	gca Ala	gac Asp	agg Arg	gtt Val 150	ctg Leu	gat Asp	gtg Val	gtg Val	gag Glu 155	agg Arg	agc Ser	ctc Leu	agc Ser	aac Asn 160	480
tac Tyr	ccc Pro	ttt Phe	gac Asp	ttc Phe 165	cag Gln	ggg Gly	gcc Ala	agg Arg	atc Ile 170	att Ile	act Thr	ggc Gly	caa Gln	gag Glu 175	gaa Glu	528
ggt Gly	gcc Ala	tat Tyr	ggc Gly 180	tgg Trp	att Ile	act Thr	atc Ile	aac Asn 185	tat Tyr	ctg Leu	ctg Leu	ggc Gly	aaa Lys 190	ttc Phe	agt Ser	576
cag Gln	aaa Lys	aca Thr 195	agg Arg	tgg Trp	ttc Phe	agc Ser	ata Ile 200	gtc Val	cca Pro	tat Tyr	gaa Glu	acc Thr 205	aat Asn	aat Asn	cag Gln	624
gaa Glu	acc Thr 210	ttt Phe	gga Gly	gct Ala	ttg Leu	gac Asp 215	ctt Leu	ggg Gly	gga Gly	gcc Ala	tct Ser 220	aca Thr	caa Gln	gtc Val	act Thr	672
ttt Phe 225	gta Val	ccc Pro	caa Gln	aac Asn	cag Gln 230	act Thr	atc Ile	gag Glu	tcc Ser	cca Pro 235	gat Asp	aat Asn	gct Ala	ctg Leu	caa Gln 240	720
ttt Phe	cgc Arg	ctc Leu	tat Tyr	ggc Gly 245	aag Lys	gac Asp	tac Tyr	aat Asn	gtc Val 250	tac Tyr	aca Thr	cat His	agc Ser	ttc Phe 255	ttg Leu	768
tgc Cys	tat Tyr	ggg Gly	aag Lys 260	gat Asp	cag Gln	gca Ala	ctc Leu	tgg Trp 265	cag Gln	aaa Lys	ctg Leu	gcc Ala	aag Lys 270	gac Asp	att Ile	816
cag Gln	gtt Val	gca Ala 275	agt Ser	aat Asn	gaa Glu	att Ile	ctc Leu 280	agg Arg	gac Asp	cca Pro	tgc Cys	ttt Phe 285	cat His	cct Pro	gga Gly	864
tat Tyr	aag Lys 290	aag Lys	gta Val	gtg Val	aac Asn	gta Val 295	agt Ser	gac Asp	ctt Leu	tac Tyr	aag Lys 300	acc Thr	ccc Pro	tgc Cys	acc Thr	912
aag Lys 305	aga Arg	ttt Phe	gag Glu	atg Met	act Thr 310	ctt Leu	cca Pro	ttc Phe	cag Gln 315	cag Gln 315	ttt Phe	gaa Glu	atc Ile	cag Gln	ggt Gly 320	960
att Ile	gga Gly	aac Asn	tat Tyr	caa Gln 325	caa Gln	tgc Cys	cat His	caa Gln	agc Ser 330	atc Ile	ctg Leu	gag Glu	ctc Leu	ttc Phe 335	aac Asn	1008
acc Thr	agt Ser	tac Tyr	tgc Cys 340	cct Pro	tac Tyr	tcc Ser	cag Gln	tgt Cys 345	gcc Ala	ttc Phe	aat Asn	ggg Gly	att Ile 350	ttc Phe	ttg Leu	1056
cca Pro	cca Pro	ctc Leu 355	cag Gln	ggg Gly	gat Asp	ttt Phe	ggg Gly 360	gca Ala	ttt Phe	tca Ser	gct Ala	ttt Phe 365	tac Tyr	ttt Phe	gtg Val	1104
atg Met	aag Lys 370	ttt Phe	tta Leu	aac Asn	ttg Leu	aca Thr 375	tca Ser	gag Glu	aaa Lys	gtc Val	tct Ser 380	cag Gln	gaa Glu	aag Lys	gtg Val	1152
act Thr 385	gag Glu	atg Met	atg Met	aaa Lys	aag Lys 390	ttc Phe	tgt Cys	gct Ala	cag Gln	cct Pro 395	tgg Trp	gag Glu	gag Glu	ata Ile	aaa Lys 400	1200
aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg 12	agt	gaa	tac	tgc	ttt	1248

Thr	Ser	Tyr	Ala	Gly 405	Val	Lys	Glu	Lys	Tyr 410	Leu	Ser	Glu	Tyr	Cys 415	Phe		
tct	ggt	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	1296	
Ser	Gly	Thr	Tyr 420	Ile	Leu	Ser	Leu	Leu 425	Leu	Gln	Gly	Tyr	His 430	Phe	Thr		
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1344	
Ala	Asp	Ser 435	Trp	Glu	His	Ile	His 440	Phe	Ile	Gly	Lys	Ile 445	Gln	Gly	Ser		
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1392	
Asp	Ala	Gly	Trp	Thr	Leu	Gly 455	Tyr	Met	Leu	Asn	Leu 460	Thr	Asn	Met	Ile		
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	taa		1437	
Pro	Ala	Glu	Gln	Pro	Leu 470	Ser	Thr	Pro	Leu	Ser 475	His	Ser	Thr				

<210> 8
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 8

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
1				5					10					15	
Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys
			20					25					30		
Lys	Thr	Gln	Leu	Thr	Ser	Ser	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn
		35					40					45			
Val	Lys	Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu
	50					55					60				
Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val
	65				70					75					80
His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe
				85					90					95	
Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu
			100					105					110		
Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val
		115					120					125			
Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu
	130					135					140				
Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn
	145				150					155					160
Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu
				165					170					175	
Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser
			180					185					190		
Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln
		195					200					205			

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235 240
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 245 250 255
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 260 265 270
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
 305 310 315 320
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
 325 330 335
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
 340 345 350
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
 355 360 365
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
 370 375 380
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
 385 390 395 400
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
 405 410 415
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
 420 425 430
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
 435 440 445
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
 450 455 460
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser
 20

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 10
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 11
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 11
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
35 40

<210> 12
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 12
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
20 25

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 13
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
20 25 30

Lys	Asp	Tyr	Lys 105	Cys	Lys	Val	Ser	Asn 110	Lys	Ala	Leu	Pro	Ala 115	Pro	Met		
cag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	440	
Gln	Lys	Thr 120	Ile	Ser	Lys	Ala	Lys 125	Gly	Gln	Pro	Arg	Glu 130	Pro	Gln	Val		
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	488	
Tyr	Thr 135	Leu	Pro	Pro	Ser	Arg 140	Asp	Glu	Leu	Thr	Lys 145	Asn	Gln	Val	Ser		
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agg	cac	atc	gcc	gtg	gag	536	
Leu	Thr	Cys	Leu	Val	Lys 155	Gly	Phe	Tyr	Pro	Arg 160	His	Ile	Ala	Val	Glu 165		
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	584	
Trp	Glu	Ser	Asn	Gly 170	Gln	Pro	Glu	Asn	Asn 175	Tyr	Lys	Thr	Thr	Pro 180	Pro		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	632	
Val	Leu	Asp	Ser 185	Asp	Gly	Ser	Phe	Phe 190	Leu	Tyr	Ser	Lys	Leu 195	Thr	Val		
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	680	
Asp	Lys	Ser 200	Arg	Trp	Gln	Gln	Gly 205	Asn	Val	Phe	Ser	Cys 210	Ser	Val	Met		
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	728	
His	Glu 215	Ala	Leu	His	Asn	His 220	Tyr	Thr	Gln	Lys	Ser 225	Leu	Ser	Leu	Ser		
ccg	ggt	aaa	tga													740	
Pro	Gly	Lys															
230																	

<210> 17
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 17
 Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15
 Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
 145 150 155 160
 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 18
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 18
 ctttccatcc tgagcaac 18

<210> 19
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 19
 aaaaaactag tcagaacaaa gctttgccag aaaacg 36

<210> 20
 <211> 24
 <212> PRT
 <213> Mus sp.

<400> 20
 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
 1 5 10 15
 Leu Val Leu Leu Pro Val Thr Ser
 20

<210> 21
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 21
 ctagttctgg agactacaaa gatgacgatg acaaaaccca gaacaa 46

<210> 22
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 22
 agctttgttc tgggttttgt catcgatc tttgtagtct ccagaa 46

<210> 23
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 23
 ccggtggac tttgggtac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctccac tccaccta 89

<210> 24
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
 ggccttaggt ggagtgggag agaggtgtgg acaatggtg ctcagctggg atcatgttgg 60
 tcaggttcag catgtagccc aaagtccag 89

<210> 25
 <211> 1464
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1461)

<220>
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 25
 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

aaa Lys	aca Thr	cag Gln 35	cta Leu	act Thr	agt Ser	tca Ser	gga Gly 40	gac Asp	tac Tyr	aaa Lys	gat Asp	gac Asp 45	gat Asp	gac Asp	aaa Lys	144
acc Thr	cag Gln 50	aac Asn	aaa Lys	gca Ala	ttg Leu	cca Pro 55	gaa Glu	aac Asn	gtt Val	aag Lys	tat Tyr 60	ggg Gly	att Ile	gtg Val	ctg Leu	192
gat Asp 65	gcg Ala	ggt Gly	tct Ser	tct Ser	cac His 70	aca Thr	agt Ser	tta Leu	tac Tyr	atc Ile 75	tat Tyr	aag Lys	tgg Trp	cca Pro	gca Ala 80	240
gaa Glu	aag Lys	gag Glu	aat Asn	gac Asp 85	aca Thr	ggc Gly	gtg Val	gtg Val	cat His 90	caa Gln	gta Val	gaa Glu	gaa Glu	tgc Cys 95	agg Arg	288
gtt Val	aaa Lys	ggt Gly	cct Pro 100	gga Gly	atc Ile	tca Ser	aaa Lys	ttt Phe 105	gtt Val	cag Gln	aaa Lys	gta Val	aat Asn 110	gaa Glu	ata Ile	336
ggc Gly	att Ile	tac Tyr 115	ctg Leu	act Thr	gat Asp	tgc Cys	atg Met 120	gaa Glu	aga Arg	gct Ala	agg Arg	gaa Glu 125	gtg Val	att Ile	cca Pro	384
agg Arg 130	tcc Ser	cag Gln	cac His	caa Gln	gag Glu	aca Thr 135	ccc Pro	gtt Val	tac Tyr	ctg Leu	gga Gly 140	gcc Ala	acg Thr	gca Ala	ggc Gly	432
atg Met 145	cgg Arg	ttg Leu	ctc Leu	agg Arg	atg Met 150	gaa Glu	agt Ser	gaa Glu	gag Glu	ttg Leu 155	gca Ala	gac Asp	agg Arg	gtt Val	ctg Leu 160	480
gat Asp	gtg Val	gtg Val	gag Glu	agg Arg 165	agc Ser	ctc Leu	agc Ser	aac Asn	tac Tyr 170	ccc Pro	ttt Phe	gac Asp	ttc Phe	cag Gln 175	ggt Gly	528
gcc Ala	agg Arg	atc Ile	att Ile 180	act Thr	ggc Gly	caa Gln	gag Glu	gaa Glu 185	ggt Gly	gcc Ala	tat Tyr	ggc Gly	tgg Trp 190	att Ile	act Thr	576
atc Ile	aac Asn	tat Tyr 195	ctg Leu	ctg Leu	ggc Gly	aaa Lys	ttc Phe 200	agt Ser	cag Gln	aaa Lys	aca Thr	agg Arg 205	tgg Trp	ttc Phe	agc Ser	624
ata Ile 210	gtc Val	cca Pro	tat Tyr	gaa Glu	acc Thr	aat Asn 215	aat Asn	cag Gln	gaa Glu	acc Thr	ttt Phe 220	gga Gly	gct Ala	ttg Leu	gac Asp	672
ctt Leu 225	ggg Gly	gga Gly	gcc Ala	tct Ser	aca Thr 230	caa Gln	gtc Val	act Thr	ttt Phe	gta Val 235	ccc Pro	caa Gln	aac Asn	cag Gln 240	act Thr 240	720
atc Ile	gag Glu	tcc Ser	cca Pro	gat Asp 245	aat Asn	gct Ala	ctg Leu	caa Gln	ttt Phe 250	cgc Arg	ctc Leu	tat Tyr	ggc Gly	aag Lys 255	gac Asp	768
tac Tyr	aat Asn	gtc Val	tac Tyr 260	aca Thr	cat His	agc Ser	ttc Phe	ttg Leu 265	tgc Cys	tat Tyr	ggg Gly	aag Lys	gat Asp 270	cag Gln	gca Ala	816
ctc Leu	tgg Trp	cag Gln 275	aaa Lys	ctg Leu	gcc Ala	aag Lys	gac Asp 280	att Ile	cag Gln	gtt Val	gca Ala	agt Ser 285	aat Asn	gaa Glu	att Ile	864
ctc Leu 290	agg Arg	gac Asp	cca Pro	tgc Cys	ttt Phe	cat His 295	cct Pro	gga Gly	tat Tyr	aag Lys	aag Lys 300	gta Val	gtg Val	aac Asn	gta Val	912
agt Glu	gac Glu	ctt Leu	tac Leu	aag Glu	acc Glu	ccc Pro	tgc Glu	acc Glu	aag Glu	aga Glu 20	ttt Glu	gag Glu	atg Glu	act Glu	ctt Leu	960

Ser 305	Asp	Leu	Tyr	Lys	Thr 310	Pro	Cys	Thr	Lys	Arg 315	Phe	Glu	Met	Thr	Leu 320		
cca	ttc	cag	cag	ttt	gaa	atc	cag	ggt	att	gga	aac	tat	caa	caa	tgc	1008	
Pro	Phe	Gln	Gln	Phe 325	Glu	Ile	Gln	Gly	Ile 330	Gly	Asn	Tyr	Gln	Gln 335	Cys		
cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	acc	agt	tac	tgc	cct	tac	tcc	1056	
His	Gln	Ser	Ile 340	Leu	Glu	Leu	Phe	Asn 345	Thr	Ser	Tyr	Cys	Pro 350	Tyr	Ser		
cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	cca	cca	ctc	cag	ggg	gat	ttt	1104	
Gln	Cys	Ala 355	Phe	Asn	Gly	Ile	Phe 360	Leu	Pro	Pro	Leu	Gln 365	Gly	Asp	Phe		
ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	atg	aag	ttt	tta	aac	ttg	aca	1152	
Gly	Ala 370	Phe	Ser	Ala	Phe	Tyr 375	Phe	Val	Met	Lys	Phe 380	Leu	Asn	Leu	Thr		
tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	act	gag	atg	atg	aaa	aag	ttc	1200	
Ser 385	Glu	Lys	Val	Ser	Gln 390	Glu	Lys	Val	Thr	Glu 395	Met	Met	Lys	Lys	Phe 400		
tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	aca	tct	tac	gct	gga	gta	aag	1248	
Cys	Ala	Gln	Pro	Trp 405	Glu	Glu	Ile	Lys	Thr 410	Ser	Tyr	Ala	Gly	Val 415	Lys		
gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	tct	ggt	acc	tac	att	ctc	tcc	1296	
Glu	Lys	Tyr	Leu 420	Ser	Glu	Tyr	Cys	Phe 425	Ser	Gly	Thr	Tyr	Ile 430	Leu	Ser		
ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	gct	gat	tcc	tgg	gag	cac	atc	1344	
Leu	Leu 435	Leu	Gln	Gly	Tyr	His	Phe 440	Thr	Ala	Asp	Ser	Trp 445	Glu	His	Ile		
cat	ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	1392	
His	Phe 450	Ile	Gly	Lys	Ile	Gln 455	Gly	Ser	Asp	Ala	Gly 460	Trp	Thr	Leu	Gly		
tac	atg	ctg	aac	ctg	acc	aac	atg	atc	cca	gct	gag	caa	cca	ttg	tcc	1440	
Tyr 465	Met	Leu	Asn	Leu	Thr 470	Asn	Met	Ile	Pro	Ala 475	Glu	Gln	Pro	Leu	Ser 480		
aca	cct	ctc	tcc	cac	tcc	acc	taa									1464	
Thr	Pro	Leu	Ser	His 485	Ser	Thr											

<210> 26
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 26
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30
 Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Lys
 35 40 45
 Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
 50 55 60

Asp₆₅ Ala Gly Ser Ser His₇₀ Thr Ser Leu Tyr Ile₇₅ Tyr Lys Trp Pro Ala₈₀
 Glu Lys Glu Asn Asp₈₅ Thr Gly Val Val His₉₀ Gln Val Glu Glu Cys₉₅ Arg
 Val Lys Gly Pro₁₀₀ Gly Ile Ser Lys Phe₁₀₅ Val Gln Lys Val Asn₁₁₀ Glu Ile
 Gly Ile Tyr₁₁₅ Leu Thr Asp Cys Met₁₂₀ Glu Arg Ala Arg Glu₁₂₅ Val Ile Pro
 Arg Ser₁₃₀ Gln His Gln Glu Thr₁₃₅ Pro Val Tyr Leu Gly₁₄₀ Ala Thr Ala Gly
 Met₁₄₅ Arg Leu Leu Arg Met₁₅₀ Glu Ser Glu Glu Leu₁₅₅ Ala Asp Arg Val Leu₁₆₀
 Asp Val Val Glu Arg₁₆₅ Ser Leu Ser Asn Tyr₁₇₀ Pro Phe Asp Phe Gln Gly₁₇₅
 Ala Arg Ile Ile₁₈₀ Thr Gly Gln Glu Glu₁₈₅ Gly Ala Tyr Gly Trp₁₉₀ Ile Thr
 Ile Asn Tyr₁₉₅ Leu Leu Gly Lys Phe₂₀₀ Ser Gln Lys Thr Arg₂₀₅ Trp Phe Ser
 Ile Val₂₁₀ Pro Tyr Glu Thr Asn₂₁₅ Asn Gln Glu Thr Phe₂₂₀ Gly Ala Leu Asp
 Leu₂₂₅ Gly Gly Ala Ser Thr₂₃₀ Gln Val Thr Phe Val₂₃₅ Pro Gln Asn Gln Thr₂₄₀
 Ile Glu Ser Pro Asp₂₄₅ Asn Ala Leu Gln Phe₂₅₀ Arg Leu Tyr Gly Lys₂₅₅ Asp
 Tyr Asn Val Tyr₂₆₀ Thr His Ser Phe Leu₂₆₅ Cys Tyr Gly Lys Asp₂₇₀ Gln Ala
 Leu Trp Gln₂₇₅ Lys Leu Ala Lys Asp₂₈₀ Ile Gln Val Ala Ser₂₈₅ Asn Glu Ile
 Leu Arg₂₉₀ Asp Pro Cys Phe His₂₉₅ Pro Gly Tyr Lys Lys₃₀₀ Val Val Asn Val
 Ser₃₀₅ Asp Leu Tyr Lys Thr₃₁₀ Pro Cys Thr Lys Arg₃₁₅ Phe Glu Met Thr Leu₃₂₀
 Pro Phe Gln Gln Phe₃₂₅ Glu Ile Gln Gly Ile₃₃₀ Gly Asn Tyr Gln Gln₃₃₅ Cys
 His Gln Ser Ile₃₄₀ Leu Glu Leu Phe Asn₃₄₅ Thr Ser Tyr Cys Pro₃₅₀ Tyr Ser
 Gln Cys Ala₃₅₅ Phe Asn Gly Ile Phe₃₆₀ Leu Pro Pro Leu Gln₃₆₅ Gly Asp Phe
 Gly Ala₃₇₀ Phe Ser Ala Phe Tyr₃₇₅ Phe Val Met Lys Phe₃₈₀ Leu Asn Leu Thr
 Ser₃₈₅ Glu Lys Val Ser Gln₃₉₀ Glu Lys Val Thr Glu₃₉₅ Met Met Lys Lys Phe₄₀₀
 Cys Ala Gln Pro Trp₄₀₅ Glu Glu Ile Lys Thr₄₁₀ Ser Tyr Ala Gly Val₄₁₅ Lys
 Glu Lys Tyr Leu₄₂₀ Ser Glu Tyr Cys Phe₄₂₅ Ser Gly Thr Tyr Ile₄₃₀ Leu Ser

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
 435 440 445
 His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
 450 455 460
 Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
 465 470 475 480
 Thr Pro Leu Ser His Ser Thr
 485

<210> 27
 <211> 464
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 27
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15
 Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro
 20 25 30
 Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr
 35 40 45
 Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly
 50 55 60
 Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser
 65 70 75 80
 Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys
 85 90 95
 Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr
 100 105 110
 Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu
 115 120 125
 Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu
 130 135 140
 Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln
 145 150 155 160
 Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys
 165 170 175
 Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn
 180 185 190
 Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln
 195 200 205
 Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala
 210 215 220
 Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser
 225 230 235 240
 23

Trp₆₅ Pro Ala Glu Lys₇₀ Glu Asn Asp Thr Gly Val₇₅ Val His Gln Val Glu₈₀
 Glu Cys Arg Val₈₅ Lys Gly Pro Gly Ile Ser₉₀ Lys Phe Val Gln Lys₉₅ Val
 Asn Glu Ile Gly₁₀₀ Ile Tyr Leu Thr Asp₁₀₅ Cys Met Glu Arg Ala Arg Glu
 Val Ile Pro₁₁₅ Arg Ser Gln His Gln₁₂₀ Glu Thr Pro Val Tyr₁₂₅ Leu Gly Ala
 Thr Ala₁₃₀ Gly Met Arg Leu₁₃₅ Leu Arg Met Glu Ser Glu₁₄₀ Glu Leu Ala Asp
 Arg Val₁₄₅ Leu Asp Val₁₅₀ Val Glu Arg Ser Leu Ser₁₅₅ Asn Tyr Pro Phe Asp₁₆₀
 Phe Gln Gly Ala Arg₁₆₅ Ile Ile Thr Gly Gln₁₇₀ Glu Glu Gly Ala Tyr₁₇₅ Gly
 Trp Ile Thr Ile₁₈₀ Asn Tyr Leu Leu Gly₁₈₅ Lys Phe Ser Gln Lys₁₉₀ Thr Arg
 Trp Phe Ser₁₉₅ Ile Val Pro Tyr Glu₂₀₀ Thr Asn Asn Gln Glu₂₀₅ Thr Phe Gly
 Ala Leu₂₁₀ Asp Leu Gly Gly Ala₂₁₅ Ser Thr Gln Val Thr₂₂₀ Phe Val Pro Gln
 Asn Gln Thr Ile Glu Ser₂₃₀ Pro Asp Asn Ala Leu₂₃₅ Gln Phe Arg Leu Tyr₂₄₀
 Gly Lys Asp Tyr Asn₂₄₅ Val Tyr Thr His Ser₂₅₀ Phe Leu Cys Tyr Gly₂₅₅ Lys
 Asp Gln Ala Leu₂₆₀ Trp Gln Lys Leu Ala₂₆₅ Lys Asp Ile Gln Val₂₇₀ Ala Ser
 Asn Glu Ile₂₇₅ Leu Arg Asp Pro Cys₂₈₀ Phe His Pro Gly Tyr₂₈₅ Lys Lys Val
 Val Asn₂₉₀ Val Ser Asp Leu Tyr₂₉₅ Lys Thr Pro Cys Thr₃₀₀ Lys Arg Phe Glu
 Met Thr₃₀₅ Leu Pro Phe Gln₃₁₀ Gln Phe Glu Ile Gln₃₁₅ Gly Ile Gly Asn Tyr₃₂₀
 Gln Gln Cys His Gln₃₂₅ Ser Ile Leu Glu Leu₃₃₀ Phe Asn Thr Ser Tyr₃₃₅ Cys
 Pro Tyr Ser Gln₃₄₀ Cys Ala Phe Asn Gly₃₄₅ Ile Phe Leu Pro Pro₃₅₀ Leu Gln
 Gly Asp Phe₃₅₅ Gly Ala Phe Ser Ala₃₆₀ Phe Tyr Phe Val Met₃₆₅ Lys Phe Leu
 Asn Leu₃₇₀ Thr Ser Glu Lys Val₃₇₅ Ser Gln Glu Lys Val₃₈₀ Thr Glu Met Met
 Lys₃₈₅ Lys Phe Cys Ala Gln₃₉₀ Pro Trp Glu Glu Ile₃₉₅ Lys Thr Ser Tyr Ala₄₀₀
 Gly Val Lys Glu Lys₄₀₅ Tyr Leu Ser Glu Tyr₄₁₀ Cys Phe Ser Gly Thr₄₁₅ Tyr
 Ile Leu Ser Leu₄₂₀ Leu Leu Gln Gly Tyr₄₂₅ His Phe Thr Ala Asp₄₃₀ Ser Trp

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
435 445
Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
450 455 460
Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470

<210> 29
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 29
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15
Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr
20 25 30
Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile
35 40 45
Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
50 55 60
Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu
65 70 75 80
Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn
85 90 95
Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val
100 105 110
Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
115 120 125
Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg
130 135 140
Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe
145 150 155 160
Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp
165 170 175
Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
180 185 190
Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala
195 200 205
Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn
210 215 220
Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly
225 230 235 240
Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp
245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn
 260 265 270
 Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val
 275 280 285
 Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met
 290 295 300
 Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln
 305 310 315 320
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro
 325 330 335
 Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly
 340 345 350
 Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn
 355 360 365
 Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys
 370 375 380
 Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly
 385 390 395 400
 Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile
 405 410 415
 Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu
 420 425 430
 His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
 435 440 445
 Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
 450 455 460
 Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 30
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 30
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu
 20 25 30
 Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
 35 40 45
 Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
 50 55 60
 Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
 65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
85 90 95
Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
100 105 110
Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
115 120 125
Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
130 135 140
Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
145 150 155 160
Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
165 170 175
Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
180 185 190
Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
195 200 205
Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
210 215 220
Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
225 230 235 240
Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
245 250 255
Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
260 265 270
Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys
275 280 285
Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
290 295 300
Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
305 310 315 320
Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
325 330 335
Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
340 345 350
Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
355 360 365
Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
370 375 380
Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
385 390 395 400
Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
405 410 415
Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
420 425 430
Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 450 455 460

<210> 31
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Ala Thr Ser Trp Gly Thr val Phe Phe Met Leu val val Ser Cys
 1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
 50 55

<210> 32
 <211> 11
 <212> PRT
 <213> artificial

<220>
 <223> linker sequence

<400> 32

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser
 1 5 10

<210> 33
 <211> 13
 <212> PRT
 <213> artificial

<220>
 <223> linker sequence

<400> 33

Gly Ala Gly Gly Ala Gly Ser Gly Gly Gly Gly Gly Ser
 1 5 10

<210> 34
 <211> 10
 <212> PRT
 <213> artificial

<220>
 <223> linker sequence

<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

<210> 35
 <211> 9
 <212> PRT
 <213> artificial

<220>

<223> linker sequence

<400> 35

Gly Thr Pro Gly Thr Pro Gly Thr Pro
1 5

<210> 36

<211> 26

<212> PRT

<213> artificial

<220>

<223> linker sequence

<400> 36

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser
20 25

<210> 37

<211> 4

<212> PRT

<213> artificial

<220>

<223> linker sequence

<400> 37

Thr Ser Ser Gly
1